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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/925,674A

DATE: 01/16/2002
 TIME: 13:23:28

Input Set : A:\11686a.asc
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ENTERED

3 <110> APPLICANT: AMRAD Operations Pty Ltd
 5 <120> TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
 6 FAMILY OF APOPTOSIS-CONTROLLING GENES
 8 <130> FILE REFERENCE: 11686a
 10 <140> CURRENT APPLICATION NUMBER: US/09/925,674A
 10 <141> CURRENT FILING DATE: 2001-08-09
 10 <150> PRIOR APPLICATION NUMBER: 09/925,674
 11 <151> PRIOR FILING DATE: 2001-08-09
 13 <150> PRIOR APPLICATION NUMBER: PN8965
 14 <151> PRIOR FILING DATE: 1996-03-27
 16 <160> NUMBER OF SEQ ID NOS: 9
 18 <170> SOFTWARE: PatentIn Ver. 2.1
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 21 <211> LENGTH: 33
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Mouse
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 27 <222> LOCATION: 16
 28 <223> OTHER INFORMATION: n is inosine
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 42 <222> LOCATION: 25
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 50 <211> LENGTH: 9
 51 <212> TYPE: PRT
 52 <213> ORGANISM: Mouse
 54 <220> FEATURE:
 55 <221> NAME/KEY: Unsure
 56 <222> LOCATION: 5
 57 <223> OTHER INFORMATION: Xaa is Ile or Val
 59 <400> SEQUENCE: 2
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 61 1 5
 64 <210> SEQ ID NO: 3
 65 <211> LENGTH: 31

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82 <223> OTHER INFORMATION: n is inosine
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96 <223> OTHER INFORMATION: Xaa is Asp or Glu
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125 <222> LOCATION: (1)..(579)
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130 1 5 10 15

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132   ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc   96
133   Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
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136   ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca   144
137   Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
138           35           40           45
140   gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg   192
141   Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
142           50           55           60
144   gcg gct cag ctg cat gtg acc cca ggc tca gcc cag cag caa cgc ttc acc   240
145   Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
146           65           70           75           80
148   cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt   288
149   Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
150           85           90           95
152   gta gcc ttc ttt gtc ttt ggg gct gca ctg tgt gct gag agt gtc aac   336
153   Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
154           100          105          110
156   aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc   384
157   Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
158           115          120          125
160   tac ctg gag acg cgg ctg gct gac tgg atc cac agc agt ggg ggc tgg   432
161   Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
162           130          135          140
164   gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg   480
165   Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
166           145          150          155          160
168   cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg   528
169   Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
170           165          170          175
172   gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc   576
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177   Lys
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181 <211> LENGTH: 193
182 <212> TYPE: PRT
183 <213> ORGANISM: HUMAN
185 <400> SEQUENCE: 7
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192   Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
193           35           40           45
195   Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
196           50           55           60
198   Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr

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199      65      70      75      80
201  Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
202      85      90      95
204  Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
205      100      105      110
207  Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
208      115      120      125
210  Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
211      130      135      140
213  Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
214      145      150      155      160
216  Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
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222  Lys
226 <210> SEQ ID NO: 8
227 <211> LENGTH: 582
228 <212> TYPE: DNA
229 <213> ORGANISM: Mouse
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (1)..(579)
235 <400> SEQUENCE: 8
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237  Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
238      1      5      10      15
240      ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggc 96
241  Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
242      20      25      30
244  cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct 144
245  Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
246      35      40      45
248  gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg 192
249  Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
250      50      55      60
252  gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
253  Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
254      65      70      75      80
256  cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt 288
257  Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
258      85      90      95
260  gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac 336
261  Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
262      100      105      110
264  aaa gaa atg gag cct ttg gtg gga caa gtg cag gat tgg atg gtg gcc 384
265  Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala
266      115      120      125
268  tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg 432

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269 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
270      130      135      140
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273 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
274      145      150      155      160
276 cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528
277 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
278      165      170      175
281 gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
282 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
283      180      185      190
285 aag tga 582
286 Lys
289 <210> SEQ ID NO: 9
290 <211> LENGTH: 193
291 <212> TYPE: PRT
292 <213> ORGANISM: Mouse
294 <400> SEQUENCE: 9
295 Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp
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297 Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
298      20      25      30
299 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
300      35      40      45
301 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
302      50      55      60
303 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
304      65      70      75      80
305 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
306      85      90      95
307 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
308      100      105      110
309 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala
310      115      120      125
311 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
312      130      135      140
313 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
314      145      150      155      160
315 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
316      165      170      175
317 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
318      180      185      190
319 Lys

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VERIFICATION SUMMARY
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DATE: 01/16/2002
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Output Set: N:\CRF3\01162002\I925674A.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4